

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 16:37:52 ; Search time 32 Seconds
(without alignments)
1674.133 Million cell updates/sec

Title: US-09-840-243B-11
Perfect score: 1341
Sequence: 1 MELTQPAEDLIQTQTPASE.....VIENHILKLFQSNLPADPE 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621.5	46.3	313	4 Q9H9E1	Q9H9E1 homo sapien
2	612.5	45.7	312	11 Q99PE2	Q99PE2 mus musculu
3	439	32.7	154	11 Q9D1J8	Q9D1J8 mus musculu
4	274	20.4	234	5 Q9VL58	Q9VL58 drosophila
5	219.5	16.4	426	16 Q8YTG9	Q8YTG9 anabaena sp
6	214	16.0	1786	5 Q17344	Q17344 caenorhabdi
7	214	16.0	1809	5 Q17487	Q17487 caenorhabdi
8	214	16.0	1815	5 Q17488	Q17488 caenorhabdi
9	214	16.0	1867	5 Q17486	Q17486 caenorhabdi
10	214	16.0	2039	5 Q17489	Q17489 caenorhabdi
11	214	16.0	6994	5 Q17343	Q17343 caenorhabdi
12	212	15.8	1762	11 Q9EQG6	Q9EQG6 rattus norv
13	212	15.8	1777	4 Q9ULH0	Q9ULH0 homo sapien
14	210.5	15.7	1159	5 Q9NCP8	Q9NCP8 drosophila
15	210.5	15.7	1599	11 Q99NH0	Q99NH0 mus musculu
16	210.5	15.7	2443	5 Q9VSA2	Q9VSA2 drosophila

17	207.5	15.5	1031	4 Q9UF42	Q9UF42 homo sapien
18	207.5	15.5	1715	11 Q9ERD4	Q9ERD4 rattus norv
19	207	15.4	598	11 Q9CUB2	Q9CUB2 mus musculu
20	206.5	15.4	552	4 Q96JF1	Q96JF1 homo sapien
21	206.5	15.4	719	4 Q96F53	Q96F53 homo sapien
22	206.5	15.4	917	4 Q96KH4	Q96KH4 homo sapien
23	205.5	15.3	342	5 Q9VQI1	Q9VQI1 drosophila
24	205	15.3	655	11 Q9CZK6	Q9CZK6 mus musculu
25	201	15.0	616	4 Q96GK0	Q96GK0 homo sapien
26	199	14.8	1498	5 Q9W211	Q9W211 drosophila
27	198	14.8	627	4 Q8WY90	Q8WY90 homo sapien
28	198	14.8	1486	4 Q8TEF1	Q8TEF1 homo sapien
29	198	14.8	4001	5 Q8WRQ7	Q8WRQ7 drosophila
30	197	14.7	686	4 Q9NXF0	Q9NXF0 homo sapien
31	197	14.7	843	11 P97582	P97582 rattus norv
32	195.5	14.6	456	10 Q9SR03	Q9SR03 arabidopsis
33	195	14.5	435	4 Q9HA95	Q9HA95 homo sapien
34	193	14.4	871	11 Q9ET47	Q9ET47 mus musculu
35	193	14.4	2622	11 Q70511	Q70511 rattus norv
36	193	14.4	4377	4 Q12955	Q12955 homo sapien
37	192	14.3	475	11 Q8VHF9	Q8VHF9 rattus norv
38	192	14.3	532	4 Q9H2U0	Q9H2U0 homo sapien
39	191	14.2	605	6 Q9GM49	Q9GM49 macaca fasc
40	191	14.2	1856	4 Q99407	Q99407 homo sapien
41	190	14.2	460	4 Q9H6J9	Q9H6J9 homo sapien
42	190	14.2	784	5 Q9VCA7	Q9VCA7 drosophila
43	189	14.1	627	4 Q96G77	Q96G77 homo sapien
44	189	14.1	1001	4 Q14349	Q14349 homo sapien
45	189	14.1	1001	4 Q9UQL8	Q9UQL8 homo sapien

ALIGNMENTS

RESULT 1

Q9H9E1 ID Q9H9E1 PRELIMINARY; PRT; 313 AA.

AC Q9H9E1; Q9H9E1; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE CDNA FLJ12814 fis, clone NT2RP2002520, weakly similar to Homo sapiens

DE transcription factor RFX-B (RFXB) mRNA (Ankyrin) (Ankyrin-repeat

DE family A protein 2) (Hypothetical 34.3 kDa protein).

GN ANKRA2.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RA [1]

RA SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto D.,

RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

RA "NEDO human cDNA sequencing project."

RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RL [2]

RL SEQUENCE FROM N.A.

RL Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,

RA Tang R., Chen X., Wu C.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RN SEQUENCE FROM N.A.

RN MEDLINE=20422473; PubMed=10965114;

RX Rader K., Boyer A.D., Farquhar M.G., Arden K.C.;

RT "Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to

RT human chromosome 5q12-->q13 by radiation hybrid mapping and somatic

RT cell hybrid PCR.";

RL Cytogenet. Cell Genet. 89:164-165(2000).

RN [4]

RN SEQUENCE FROM N.A.

RA Rader K.A., Orlando R.A., Lou X., Farquhar M.G.;
RT "Characterization of ANKRA, a novel ankyrin repeat protein that
interacts with the cytoplasmic domain of megalin.";
RL J. Am. Soc. Nephrol. 11:0-0(2001).
RN [5]

RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022876; BAB14288.1; -
DR EMBL; AF251051; AAK34941.1; -
DR EMBL; AF314032; AAK01621.1; -
DR EMBL; BC012917; AAK12917.1; -
DR HSSP; P80144; 2MYO.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat, Hypothetical protein; Repeat.
SQ SEQUENCE 313 AA; 34272 MW; 31C653B10B4ED6E1 CRC64;

Query Match 46.3%; Score 621.5; DB 4; Length 313;
Best Local Similarity 60.6%; Pred. No. 2.9e-44;
Matches 126; Conservative 26; Mismatches 49; Indels 7; Gaps 2;
QY 51 NPEPDASV-----SSPQAGSSLKSHSTLTNRQGNESALPATLDSLSIHQLAQQELD 104
Db 104 SPSFGIOVRHVYTPSTTKHFSPIKQSTLTNKHGNEVSTPLLANSLSHQLAQQEML 163
QY 105 QLKEHLRKGDNLVKNKPDREGFPLIMASAFGEIETVRFLLEWGADPHILAKERESALS 164
Db 164 YLATRIEQ-ENVINHTDEEGFTPLMMAAHQIAVEFLLONGADPQLLGKRESALS 222
QY 165 STGYTDIVGLLERVDINIDYDNGGTPLLYAVRGNVKCVKVEALLARGADLTTEADSGY 224
Db 223 CSKGYTDIVKMLDGCVDVNEYDNGGTPLLYAVHGNHVKCVKMLLESADPTIETDSGY 282
QY 225 TPMDLAVALGYRKVQVQVIEHNLKLFQS 252
Db 283 NSMDLAVALGYRSVQVQVIESHLKLQN 310

RESULT 2

ID Q99PE2 PRELIMINARY; PRT; 312 AA.
AC Q99PE2;

DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE Ankyrin-repeat family A protein.
DE ANKRA2 OR 110004M18RIK.

GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20422473; PubMed=10965114;

RA Rader K., Boyer A.D., Farquhar M.G., Arden K.C.;
RT "Assignment of ankyrin repeat, family A (RFXANK-like) 2 (ANKRA2) to
human chromosome 5q12-->q13 by radiation hybrid mapping and somatic
cell hybrid PCR.";
RL Cytogenet. Cell Genet. 89:164-165(2000).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=20547411; PubMed=11095640;

RA Rader K., Orlando R.A., Lou X., Farquhar M.G.;
RT "Characterization of ANKRA, a novel ankyrin repeat protein that
interacts with the cytoplasmic domain of megalin.";
RL J. Am. Soc. Nephrol. 11:2167-2178(2000).
DR EMBL; AF314031; AAK01620.1; -

DR HSSP; P80144; 2MYO.
DR MGD; MGI:1915808; Ankra2.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat, Repeat.
SQ SEQUENCE 312 AA; 34062 MW; 3B52B1415B7A5AFA CRC64;

Query Match 45.7%; Score 612.5; DB 11; Length 312;
Best Local Similarity 60.1%; Pred. No. 1.7e-43;
Matches 125; Conservative 25; Mismatches 51; Indels 7; Gaps 2;

QY 51 NPEPDASV-----SSPQAGSSLKSHSTLTNRQGNESALPATLDSLSIHQLAQQELD 104
Db 103 SPSFGIOVRHVYTPSTTKHFSPIKQSTLTNKHGNEVSTPLLANSLSHQLAQQEML 162
QY 105 QLKEHLRKGDNLVKNKPDREGFPLIMASAFGEIETVRFLLEWGADPHILAKERESALS 164
Db 163 YLATRIEQ-ENVINHTDEEGFTPLMMAAHQIAVEFLLONGADPQLLGKRESALS 221
QY 165 STGYTDIVGLLERVDINIDYDNGGTPLLYAVRGNVKCVKVEALLARGADLTTEADSGY 224
Db 222 CSKGYTDIVKMLDGCVDVNEYDNGGTPLLYAVHGNHVKCVKMLLENGADPTIETDSGY 281
QY 225 TPMDLAVALGYRKVQVQVIEHNLKLFQS 252
Db 282 NSMDLAVALGYRGVQVQVIESHLKLQN 309

RESULT 3

ID Q9D1J8 PRELIMINARY; PRT; 154 AA.
AC Q9D1J8;

DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE 110004M18RIK protein.
DE ANKRA2 OR 110004M18RIK.

GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyndon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003438; BAB22790.1; -

DR HSSP; P80144; 2MYO.
DR MGD; MGI:1915808; Ankra2.
DR InterPro; IPR002110; ANK.

RL DNA Res. 8:205-213(2001).
DR EMBL; AP003590; BAB74447.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 13.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 13.
DR PROSITE; PS50088; ANK_REPEAT; 11.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 426 AA; 43800 MW; CF0B9E5D43ACAA03 CRC64;

Query Match 16.4%; Score 219.5; DB 16; Length 426;
Best Local Similarity 30.7%; Pred. No. 3.5e-10;
Matches 62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;

QY 62 QAGSSLKSTTL-----TNRQGNESVALPATLDSLSIHQLAAGELDQLK 107
DB 234 QDGSALHLATVEGYVDVQVLLNGANTQIKNKLGDTPLVAALQGH-----DQIV 285
QY 108 EHLRK-----GDNLVKNPDERGFTPLIWASAFGEIETVRFLEWGADPHILAKERESAL 161
DB 286 ETLKYGANVHGDNL-----GETPLTLAASQGHATATVRILLDYGANANIPASDGKTAL 338
QY 162 SLASTGYTDIVGLLERVDINITYDMNGTPLLVAVRGNHVKEALLARGADLTTEAD 221
DB 339 IKATERNHPGVIOQLLAKGANVNYQDSVGATALLIWAASGYNKVVQILLLEGADTNLKNR 398
QY 222 SGYTPMDLAVALLGYRKVOQVIE 243
DB 399 GGYTALMIAEFNGFRSIVQILK 420

RESULT 6

Q17344 PRELIMINARY; PRT; 1786 AA.
ID Q17344;
AC Q17344;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE UNC-44 (Fragment).
GN UNC-44.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=95263663; PubMed=7744957;
RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
RA Boontrakulpoontawe P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
RA Sobery A.;
RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
RT guidance in Caenorhabditis elegans.";
RT J. Cell Biol. 129:1081-1092(1995).
DR EMBL; U21734; AAA85854.1; -.
DR HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
FT NON_TER 1786 1786

SQ SEQUENCE 1786 AA; 195550 MW; 03E220FB521747F1 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1786;
Best Local Similarity 27.3%; Pred. No. 8.7e-09;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDPGEAEADGSDTVVLSLPCTPEPVNPPEPDASVSSPQAGSSLKSTTLNRR 78
DB 2 SNEGDPFPQOQOPESEVOA----PAPEPGRAE----- 32
QY 79 GNEVSALPATLDSLSIHQLAAGELDQLKEHLRKGDNLVKNPDERGFTPLIWASAFGEIE 138
DB 33 -----GSASFURARAGDLEKVELLRAGTD-INTSNANGLNSLHLASKEGHSE 80
QY 139 TVRFLEWGADPHILAKERESALSLASTGYTDIVGLLERVDINITYDMNGTPLLAV 198
DB 81 VRELIRKQAOVDAATRKGNLTALHIASLAGQSLIVTLVENGANVNVQSVNGFTPLYMAA 140
QY 199 RGNHVKEALLARGADLTTEADSGYTPMDLAVALLGY-RKVQCVTEN 244
DB 141 QENHEEVKYLKKGANQALSTEDGFTPLAVALLQOQHDRVAVVLLLEN 187

RESULT 7

Q17487 PRELIMINARY; PRT; 1809 AA.
ID Q17487;
AC Q17487;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE E. elegans ankyrin-related unc-44 (GB:U21734).
GN UNC-44.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RA [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RT Nature 368:32-38(1994).
RL [2]
RP SEQUENCE FROM N.A.
RA Gatlung S.;
RT "The sequence of C. elegans cosmid B0350.";
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50071; AAA93446.1; -.
DR HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.


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DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SQ SEQUENCE 1809 AA; 198193 MW; AD86349AA64534F8 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1809;
Best Local Similarity 27.3%; Pred. No. 8.9e-09;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDPGEAADGSDTVVLSLPCTPEPVNPEPDASVSSPQAGSSLKSTLTNRQR 78
   ||| : : : : : |||
DB 2 SNEGDPQPQQQPESQEVQ-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLHQAQGLDQKHLRKGDNLVKNPDERGFTPLIWASAFGEIE 138
   ||| : : : : : |||
DB 33 -----GSASFLRAARAGDLEKVELLRAGTD-INTSNANGLSLHLASKEGHS 80

QY 139 TVRFLEWGADPHILAKERESALSTAGYTDIVGLLLEKVDVINYDWNNGTPLLAV 198
   ||| : : : : : |||
DB 81 VVRELKRAQAVDAATRKGNLTALHTASLAGQSLIVTLVENGANVNVQSVNGFTPLVMAA 140

QY 199 RGNHVKVEALLARGADLTTEADSGYTPMDLAVAGY-RKVQOVIE 244
   ||| : : : : : |||
DB 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQGGHDRVAVLLEN 187

RESULT 8
Q17488 PRELIMINARY; PRT; 1815 AA.
AC Q17488; 002517;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE C. ELEGANS ankyrin-related UNC-44 (GB:U21734).
GN UNC-44.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCB1_TaxID=6239;
OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Gattung S.
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=N2;
RX MEDLINE=95263663; PubMed=7744957;
RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
RA Boontrakulpoontawe P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,
RA Sobery A.
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RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
RT guidance in Caenorhabditis elegans."
RL J. Cell Biol. 129:1081-1092(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Otsuka A.J.
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Otsuka A.J.
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50071; AAA93445.1; -.
DR EMBL; U39847; AAB41826.1; -.
DR HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH 1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZUS; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SQ SEQUENCE 1815 AA; 198956 MW; 3ECC6E310915C915 CRC64;

Query Match 16.0%; Score 214; DB 5; Length 1815;
Best Local Similarity 27.3%; Pred. No. 8.9e-09;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDPGEAADGSDTVVLSLPCTPEPVNPEPDASVSSPQAGSSLKSTLTNRQR 78
   ||| : : : : : |||
DB 2 SNEGDPQPQQQPESQEVQ-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLHQAQGLDQKHLRKGDNLVKNPDERGFTPLIWASAFGEIE 138
   ||| : : : : : |||
DB 33 -----GSASFLRAARAGDLEKVELLRAGTD-INTSNANGLSLHLASKEGHS 80

QY 139 TVRFLEWGADPHILAKERESALSTAGYTDIVGLLLEKVDVINYDWNNGTPLLAV 198
   ||| : : : : : |||
DB 81 VVRELKRAQAVDAATRKGNLTALHTASLAGQSLIVTLVENGANVNVQSVNGFTPLVMAA 140

QY 199 RGNHVKVEALLARGADLTTEADSGYTPMDLAVAGY-RKVQOVIE 244
   ||| : : : : : |||
DB 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQGGHDRVAVLLEN 187

RESULT 9
Q17486 PRELIMINARY; PRT; 1867 AA.
AC Q17486; 002516;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE C. ELEGANS ankyrin-related UNC-44 (GB:U21734).
GN UNC-44.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCB1_TaxID=6239;
OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
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RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Gattung S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95263663; PubMed=7744957;
RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,
RA Boontrakulpoontawe P., Jeyapirakash A., Hedgecock E., Wheaton V.I.,
RA Sobery A.;
RT "An ankyrin-related gene (unc-44) is necessary for proper axonal
RT guidance in Caenorhabditis elegans.";
RL J. Cell Biol. 129:1081-1092(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Otsuka A.J.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Otsuka A.J.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN EMBL; U50071; AAA93444.1; -.
DR EMBL; U39847; AAB41828.1; -.
DR HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SQ SEQUENCE 1867 AA; 204253 MW; 4689A2104623B4C6 CRC64;
Query Match 16.0%; Score 214; DB 5; Length 1867;
Best Local Similarity 27.3%; Pred. No. 9.3e-09;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;
QY 19 SELGDPEDGEEAAGSDTVVLSLPCTPEPVNPEPDASVSSPQAGSSLKHSITLLTNQR 78
Db 2 SNEGDPFQFOQQPESQEVQ-----PAPEPGRAE----- 32
QY 79 GNEVSALPATLDSLSIHLAAGELDLQKEHLRKGDNLVKNPDERGFTPLTWASAFGEIE 138
Db 33 -----GSASFRLARAGDLEKVELLRAGTD-INTSNANGLSLHLASKEGHS 80
QY 139 TVRFLEWGAADPHILAKERESASLASTGTYTDIVGLLLERVDVINYWNGGTPLLYAV 198

Db 81 VVRELIRQAQVDATRKGNLTALHSLAGSLIVTILVENGANVQSVNGFTPLYMAA 140
QY 199 RGNHYKCEALLARGADLTTEADSGYTPMDLVALGY-RKVQOVIEN 244
Db 141 QENHEEVKYLKKGANQALSTEDGFTPLVALQGGHDRVAVVLEEN 187
RESULT 10
Q17489
ID Q17489 PRELIMINARY; PRT; 2039 AA.
AC Q17489;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE C. elegans ankyrin-related unc-44 (GB:U21734).
GN UNC-44.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Gattung S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN EMBL; U50071; AAA93443.1; -.
DR HSSP; P42773; 11HB.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001360; GH_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PRO1415; ANKYRIN.
DR PRINTS; PRO1574; TUBBYPROTEIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 22.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.
KW ANK repeat; Repeat.
SQ SEQUENCE 2039 AA; 222850 MW; 7722C4C2E6AFD68A CRC64;
Query Match 16.0%; Score 214; DB 5; Length 2039;
Best Local Similarity 27.3%; Pred. No. 1.1e-08;
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;
QY 19 SELGDPEDGEEAAGSDTVVLSLPCTPEPVNPEPDASVSSPQAGSSLKHSITLLTNQR 78

Db 2 SNEGDPPOQOQOPESEVQA-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQIAOGELDQKHLRKGDNLVKNKPDERGFTPLIWASAFGEIE 138

Db 33 -----GSASFRLARARAGDLEKVELLELRAGTD-INTSNANGLSLHLASKEGHS 80

QY 139 TVRFLEWGADPHILAKERESALSLASTGYTDIVGLLTERDVIDINIIDWNGGTPLLYAV 198

Db 81 VVRELKIQQAQVDAATRKGNLTALHIALAGOSLIVTILVENGANVNVQSVNGFTPLYMAA 140

QY 199 RGNHVKCEVALLARGADLTTEADSGYTPMDLAVALGY-RKVQOVIEH 244

Db 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOGHDRVAVLLEN 187

RESULT 11

Q17343 PRELIMINARY; PRT; 6994 AA.

AC Q17343;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE UNC-44 ankyrins.

GN UNC-44.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N2;

RX MEDLINE=95263663; PubMed=7744957;

RA Otsuka A.J., Franco R., Yang B., Shim K., Tang L.Z., Zhang Y.,

RA Boontrakulpoontawe P., Jeyaprakash A., Hedgecock E., Wheaton V.I.,

RA Sobery A.,

RT "An ankyrin-related gene (unc-44) is necessary for proper axonal

RT guidance in Caenorhabditis elegans.";

RL J. Cell Biol. 129:1081-1092(1995).

RN [2]

RP REVISIONS, AND SEQUENCE OF 6126-6994 FROM N.A.

RC STRAIN=N2;

RA Otsuka A.J.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U39847; AAB41827.1; -.

DR EMBL; U21733; AAB38384.1; -.

DR HSSP; P42773; 1IHB.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000488; Death.

DR InterPro; IPR001360; GH 1.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR000906; ZUS.

DR Pfam; PF00023; ank; 24.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00791; ZUS; 1.

DR PRINTS; PR01415; ANKYRIN.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00248; ANK; 21.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00218; ZUS; 1.

DR PROSITE; PS50088; ANK_REPEAT; 22.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_2.

KW ANK repeat; Repeat.

SEQUENCE 6994 AA; 775364 MW; 90CB449925D9923D CRC64;

Query Match 16.0%; Score 214; DB 5; Length 6994;

Best Local Similarity 27.3%; Pred. No. 6.8e-08;

Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;

QY 19 SELGDPEDGEEADSDTVVLSLPCTPEPVNPEPDASVSSPQAGSLKSTLTNRQR 78

Db 2 SNEGDPPOQOQOPESEVQA-----PAPEPGRAE----- 32

QY 79 GNEVSALPATLDSLSIHQIAOGELDQKHLRKGDNLVKNKPDERGFTPLIWASAFGEIE 138

Db 33 -----GSASFRLARARAGDLEKVELLELRAGTD-INTSNANGLSLHLASKEGHS 80

QY 139 TVRFLEWGADPHILAKERESALSLASTGYTDIVGLLTERDVIDINIIDWNGGTPLLYAV 198

Db 81 VVRELKIQQAQVDAATRKGNLTALHIALAGOSLIVTILVENGANVNVQSVNGFTPLYMAA 140

QY 199 RGNHVKCEVALLARGADLTTEADSGYTPMDLAVALGY-RKVQOVIEH 244

Db 141 QENHEEVVKYLLKHGANQALSTEDGFTPLAVALQOGHDRVAVLLEN 187

RESULT 12

Q9EOG6 PRELIMINARY; PRT; 1762 AA.

AC Q9EOG6;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE KIDINS220.

GN KIDINS220.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20568256; PubMed=10998417;

RA Iglesias T., Cabrera-Poch N., Mitchell M.P., Naven T.J., Rozengurt E.,

RA Schiavo G.,

RT "Identification and cloning of Kidins220, a novel neuronal substrate

RT of protein kinase D.";

RL J. Biol. Chem. 275:40048-40056(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Schiavo G.;

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Mitchell M., Schiavo G.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF239045; AAG35185.2; -.

DR HSSP; P80144; 2MYO.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 12.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 11.

DR PROSITE; PS50088; ANK_REPEAT; 10.

KW ANK repeat; Repeat.

SEQUENCE 1762 AA; 195715 MW; 0CB2689A571F8AE4 CRC64;

Query Match 15.8%; Score 212; DB 11; Length 1762;

Best Local Similarity 34.0%; Pred. No. 1.3e-08;

Matches 50; Conservative 34; Mismatches 61; Indels 2; Gaps 2;

QY 100 OGELDQKHLRKGDNLVKNKPDERGFTPLIWASAFGEIETVRFLEWGADPHILAKERES 159

Db 81 EGHIIIVELLKSGASLEHR-DMGGWTALMWACYKGRDVELLSHGANSVTGLYSYV 139

QY 160 ALSLASTGYTDIVGLLTERDVIDINIIDWNGGTPLLYAVRGNHVKCEVALLARGADLTTE 219

Db 140 PIWAAGRGHADIVHLLQNGAKVNCSDKYGTPPLVWAARKGHLKLVKHLAMGADVDOE 199

QY 220 ADSGYTPMDLAVALGY-RKVQOVIEH 245

Db 200 GANSMTALIVAVKGYTQSVKEILKRN 226

RESULT 13

Q9ULH0 PRELIMINARY; PRT; 1777 AA.

ID Q9ULH0

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AC Q9ULH0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA1250 protein (Fragment).
GN KIAA1250.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
DR EMBL; AB033076; BAA86564.2; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 12.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 11.
DR PROSITE; PS50088; ANK_REPEAT; 10.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON TER 1 1
SQ SEQUENCE 1777 AA; 197209 MW; B6505923FB45F143 CRC64;

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Query Match      15.8%; Score 212; DB 4; Length 1777;  
Best Local Similarity 34.7%; Pred. No. 1.3e-08;  
Matches 51; Conservative 33; Mismatches 61; Indels 2; Gaps 2;  
  
QY 100 QGELDQLKEHLRKGDNLVKNKPDERGFTPLIWASAFGEIETVRFFLEWGAADPHILAKERES 159  
   | : :: | : | : | : | : | : | : | : | : | : | :  
Db 87 EGHVHIVEELLKCGVNLEHR-DMGGMTALMWACYKGRTDVVELLSHGANSPTSGLYSVY 145  
  
QY 160 ALSLASTGYTDIVGLLTERDVIDINITYDWNGSTPLLVAVRGNHVKCVEALLARGADLTTE 219  
   | : | : | : | : | : | : | : | : | : | : | : | :  
Db 146 PIWAAGRHADIVLLTLQCAKYNCSDKYGTTPLVMAARKGHLCVKHLLAMGADVDOE 205  
  
QY 220 ADSGYTMDLAVALGY-RKVQCVIENH 245  
   | : | : | : | : | : | : | : | : | : | : | : | :  
Db 206 GANSM TALIVA VKGYTQS VXEILKEN 232  
  
RESULT 14  
Q9NCP8  
ID Q9NCP8 PRELIMINARY; PRT; 1159 AA.  
AC Q9NCP8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
Ankyrin 2.  
ANK2 OR CG7462.  
GN Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20304926; PubMed=10844021;  
RA Bouley M., Tian M.-Z., Paisley K., Shen Y.-C., Malhotra J.D.,  
RA Hortsch M.;  
RT "The U1-type cell adhesion molecule neuroglian influences the  
RT stability of neural ankyrin in the Drosophila embryo but not its  
RT axonal localization."  
RL J. Neurosci. 20:4515-4523(2000).  
DR EMBL; AF190635; AAF73309.1; -.  
DR HSSP; P42773; IINH.  
DR FlyBase; FBgn0017645; Ank2.
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[illegible]

RESULT	15
Q99NHO	
ID Q99NHO	PRELIMINARY; PRT; 1599 AA.
AC Q99NHO;	
DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
GN Gene trap ankryrin repeat containing protein. GTAR.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxId=10090; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=129/SV; RA Watt A.J., Jones E.A., Ure J., Peddie D., Wilson D., Forrester L.M.; RT "A gene trap integration provides an early in situ marker for hepatic RT specification of the foregut endoderm." RL Mech. Dev. 100(2):205-215(2001). DR EMBL; AY026253; AAK07672.1; -. DR HSSP; P42773; ITHB. DR MGD; MGI:1932101; Gtar. DR InterPro; IPR002110; ANK. DR Pfam; PF00023; ank; 25. DR PRINTS; PR01415; ANKYRIN. DR SMART; SM00248; ANK; 25. DR PROSITE; PS50088; ANK_REPEAT; 20. DR PROSITE; PS50297; ANK_REP_REGION; 1. KW ANK repeat; Repeat. SQ SEQUENCE 1599 AA; 170271 MW; CCB6C56D8ECB7C8 CRC64;	
Query Match	15.7%; Score 210.5; DB 11; Length 1599;
Best Local Similarity	29.5%; Pred. No. 1.5e-08;
Matches 71; Conservative 43; Mismatches 98; Indels 29; Gaps 8;	
OY 10 LIQTQQ-----TPASELGDPEDP----GEFAADGSDTVVLSLFPCTPEPVNPEDASVSS 60	
: : : :	
DB 999 LFTETQGGLWVASPAQTLLNDTLDDIMAVSGRASAMSNTPHTSHIAASVSQPQTPTP-SPIIS 1057	
: : : : : : : : : : : :	
OY 61 PQAGSSLKHSTLTLLNRQRGNEVSALPATLDLSIHQLAAQGELDQLKEHLRKGDNLVNKP 120	
: : : : : : : : : : : :	
DB 1058 PSAMLPIYPAYDAIDDAQTESNHDTAL-----TLACAGGHELVQTLLERGASIEHR 1107	
: : : : : : : : : : : :	
OY 121 DERGFPLIWSAFGEIETVRFLLEWGADPHILA-KERESALSASTGGYTIVIGLLLR 179	

Db 1108 DKKGFTPLILATAAGHVVEILLDNGADIEAQSERTKDTPLSLACSGGRQEVVELLAR 1167
QY 180 DVD--INIYDWNCGTPLLAVRGNHVKCVEALLARGADLTTEADS--GYTPMDLAVALG 234
Db 1168 GANKEHRNVSDY--TPLSLAASGGYVNIKILNAGAEINSRTGSKLGISPLMLAMNG 1224
QY 235 Y 235
Db 1225 H 1225

Search completed: March 17, 2003, 16:40:42
Job time : 39 secs

